# REPLACEMENT DRAWING

### FIGURE 3A

#### CITIA BOSCIO BAGRICIA POLICITA CA TOA ROBOCOGOTO COGOGO GOBOGO BOGO BOCO BOTO BOGO GOGO GOGO GOBOGA COGO CA CA CA COMO COGO GOGO BOTO BOTO BOTO COMO BOTO CO A TGGCOGAGCTGCGCCTGAAGGCCGCCAGCAACACAGGGAGTGTGTTCCCGTGCCCACCTOCGAGCACGTGGCCGAGATCGTGGGCAAGGCTGCAAGGTTAAGGC ATGECOBAGCTGCGCCTGAAGGCGGCLAGCAACACACGGAGTGTGTTCCCGGTGCOCAOCTOCGAGCGGAGATCGTGGCCAAGATCGTGGGCAAGGTAAGGTAAGGTTAAGGC ATGGCCGAGCTGCGCCTGAAGGGCAGCAGCAACACACGGAGTGTGCGGTGCCCACCACCACCACGAGGCGGAGGGGCGAAGGCAGGGCAAGGCTGCAAGGTAAGGTTAAGGC A TOBCOBACCTGCCCCTGAA GGGCACCACCACCACCACGCACTGTGTTCCCGTGCCCACCTCCGACCTGCCCAAGATCGTGCGGCAGCCAAGCTGCAAGATTAAGGC ATGGCCGAGCTGCGCCTGAAGGGCAGCAGCAACAACAACAAGGAGTGTTTCCGGTGCCCACCTCCGAGCAGGTGGCCGAGATCGTGGGCAAGGTAGGCTGCAAGATTAAGGC ATGECCEAGCTGCGCCTGAAGGCCAGCAGCAACACGGAGTGTGTTCCCGTGCCCACCTOCGAGCACGTGGCCGAGACGTGGGCAGGCAAGGCTGCAAGGTTAAGGA 222222 (333) (308) (333) MCSOALS BCY I MCSOA6 BCY I MCSOA8 BCY I MCSOA2 BCY I MOSORIS BOY I MO55.29 BCY I MO55.32 BCY I MCSOA6 BCY I MC50A8 BCY I MC54,21 BCY I Consensors original BCY1 MC55.29 BCY I original BCY1

MC55.32 BCY I

Consensus

TOTCAGCAGCAGCACTICTCCATAATCCGTGCCTCCGGCAACAAGTCAGGCGCCGCCTTTGGTGTGGCTCCTGCTTTGCCGGCCAGGTGACCATCGGTG TOTCAGCAGCAGCACTICTCCATAATCGTGCCTCCGGCAACAAGTCAGGCGCCGCCTTTGGTGTGGCTCCTGCTTTGCCCGGCCAGGTGACCATCGGTG TOTCAGCAGCAGCACTICTCCATAATCGTGCCTCCCGGAAGAAGAAGAGGCGCCGCTTTGGTGTGGCTCCTGCTTGCCTGGGGAAGTGAGCTAGGTGACCATCGTGTGCGGG ICICAGGAGGGGAGTACTTCCATGATGGGGGTOCCTOCGGAAGAAGAAGGGGGCGTTTGGTGGGGGGGTTCTGCCTGTTGCCGGGCAAGTGACGATCGGTG TOTCAGCAGCAGCACTICTCCATAATCGGTGCCTCCCGAAGAAGAAGGCGCCGCCTTTGGTGTGGCTCCTGCTTTTGCCCGGCCAGGTGACGATG TOTCAGCAGCAGCACTICTCCATGATCCGFGCCTCCCGGAACAAGTCAGGCGCCGCTTTGGTGTGGCTCTGCCTGTGCCGGCCAGGTGACCATCGTGTCGGGTG COCTACCECTECTES GECTISSTISSISCECCE DA A GOEG CAACCAATCOACCACOBORGOA AACCAA CACATA TAA TOA CACAAGOOSTOACCAGOOG C 

TOTCAGCAGCAGCACTICTCCATAATCCGTGCCTCCCGCAACAAGTCAGGCGCCGCCTTTGGTGTGGCTCCTGCTTTGCCCGGCCAGGTGACCATCGGTGACGTG

COCTACCOSTIGITICITICITICITIC COCCORAA GOGOCAA CCATCAA GOGOTATICA A COLA A COLA TRATORITA TO A CATOA A GOOGITA CO COT

(331)

Consensus

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MC55.29 BCY I MC55.32 BCY I

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MOSORIS BOY I

original BCY1 MCSOA6 BCY I MCSGAS BCY I

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(222)

Consensus

MC55.32 RCX I

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(221) (221) (221)

MCSOAS BCY I

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(222)

original BCY1 MCSOA19 BCY I

FIGURE 3B	.~.	(44)) ETREBBRICHONOLAGERACH GEBOURT GEBOURT GEBOURT GEBOURT GEBOURCH GOSCHOUS GEBOURT GEBOURT GEBOURT GEBOURT 1771 Gebourt Bourt Bourt Gebourt	· .	~ .		~	(441) STITERBRITACBOSTOCCCROSCAROSTOSROCSISCSCERGBRGRITCGRACBOCATECCESTECCECACTESCARGRITCSTCBRGTACRACRATGRARACGAST	(441) STITCEABATTAGGGTGCCCTAGGCAACGTGGAGCGTGCGCGAGGAGAATTGAGAGAGA	551		(851) TUCTEGUGGEGASOCOGAGGARUANTGATAGUGGTAUTCEGAUGGUTSGOSGGTGCAGGOOSGCTGCAAGUCOCTUTOUACUTTUGGGAAAAAACTGGGC	(851) TOCTEGLEGEGRACOCOGRACICARTGRATACCOGLIACTCEGACGCTEGGCTGGACACACACAGCOCGGCTGCAAGCOCTETCCACCTTCGGGAAAAAACTGGG	(851) TOCTEGIGGEGASCOCGACGAAGTATGATAGTCGGATATTCGGATGCTTSGCSGGTGCACCCGGCTGCAAGTCCTACCCATTCGGGAAAAAAACTGGGC	(851) TOCTEGIGGEGARCCOGACCARCARTGATAGCCGCTATTCCGACGCTEGGCTGGACGCACGCAGCCCGGCAAGCCCCTTTCCACCTTCGGAAAAAAACTGGBC	1881) TOCTEGISGEGAROCOCGROSOARTCRATACOGGIZACTCTSGCOTEGCOTEGCTOCCACOCAGOOGEGCTGCAAGOOCOTACOCACTTOGGOAGAACASOCTGGA	[551] TCCTGGGGGGGGCCCGAGGAATGATGGCGGTACTCCGAGGCTSGCGGGGGCACACACAGCGGGCTGCAAGTCCCTCTCCACCTTCGGGAAAAAAGGCTGGGC	551) TOCTGGGGGGGGGGGGGGGGGGGARCARTGGRGGGGTACCGGTGGCGTGGC	320		.~.	(661) TGCATCGGCGAGTGCGGAGTGCTGGGCTTTGAGGCCCCACGCCTGGGTGAGCAGGGGGGGG	(661) TOCATCGGCGAGTGCGGAGTGCTGGGCTTTGAGGCCCCACGCTGGGTGAGCAGGGGGGGG	(661) TBCATCBGCBAGTGCBGAGTBCTCTGGCTTTGABGCCCCACBCCTGGTBAGCAGBGGCBGBGACTTTGGCTACGBTGGGTACGBGTATTCCGGBGCTATBGCGTGBGCAA	(661) TBOATOBGOBAGTGOBGAGTGCTGGGTTTTGABGCCCCACBOCTGGBTBAGCAGBGGBGBGCTTTGGGTTACGGGTACGGTAC	(661) TBOATOBGOBAGTGOBGABTSGACTCTGGGTTTTGABGCCCCACBOCTGGBTBAGCAGBGGBGBACTTTGGGTTACGBGTACCTCTTTCCGBBGTATBGCGTGBGCAA	(651) TBCATCBGCBAGTGCBGABTBGACTCTGGCTTTTGABGCCCCTACBCTTGAGCAGBGCGGGBBACTTTGGCTACGGCTGGGTACTCTTTCCGGGGTATTBGCGTGBGCAA	771	(188) coassatgretactacceccacaactascoccccctttacasssassassassassassassassassassassastactcatakoctoctoctoctoctoct	(771) BOABBATSTBARATACGBOGTGGCCGAATAAGCCCCCCGCTGTGBBCCBBCCAABAAAGCCAACBCCAACGTCCTCTTCTCTCTTTTTCTCTTTTTTCTTCTTCTTCTT	(771) COAGGATGAGAATAAGGGGGGGGGGGGGAGTAGCCCCCCCCTGTGGGCGGGC	(771) BOABBATGABTACTACGBOGTGGCCGGAATTAGCCCCCCGTTGTGBBCGAGACGCABGABAACGCCACCACCACCTCCTTCTTCTCTTTTTCTCTCTCTC	(71) COMPONIGIBRATIACGSCGTGGCCGGGGGGGGGGCCCCCCCGTTGTGGGCGAGGGGGAAACGCCACCACCACCTCCGTGTTTTTCTCCTCTGTGCTGCTGCTCCTCTT			771) SCASSATGTSTACTSCCTGCCGCGCGCCCCCCCCCCCCCC
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	original BCY1	MCSUALS MCX			MC54.21 MC7	MC22,23 BCX	MC55.32 BCX	Consensus		original BCY1	MCSOAl9 BCY	MCSOR6 BCX	MCSOAS BCY	MC54.21 BCY	MC55.29 BCX	MC55.32 BCX	Consensus		original BCY1	MC50al9 RCY	MCSOA6 BCX	MCSOAS BCX	MC54.21 BCX	MC55.29 BCX	MC55.32 BCX	Consensus		original BCF1	MC50819 RCK	MCSOA6 RCX	MC50A8 BCY	MC54.21 BCY	MC55.29 RCY	MC55.32 BCK	Consensus

FIGURE 3B

# FIGURE 3C

### 1211  CTYPTOCORA GEOCOCOCOCOCOCOCOCOCOCOCOCOCOCOCOCOCOCOC	
	(1221)
OTIGINAL BOYL WCSOALS BOY I WCSOALS BOY I WCSOALS BOY I WCSOALS BOY I WCSS.22 BOY I WCSOALS BOY I	Consensus

9%

## FIGURE 3D

SMIRASRNKS RIGKILEYNN YYGVAETSPP GPPCAHRSPA TSAGPELAGI PRRPPGEPLQ GFSKIGGGGI RSPGGGRDCM VCFESEVTAA REIISAAEHF PGYGVGKQDV REEIETHIAV OCCRIRALRA KINTYIKTPV RGEEPVEMVT GRREDVATAR CIGECGVDSG FEAPRIGEQG GDFGYGGYLF QQTNTYIITP SRDRDPVFEI TGAPGNVERA PKGATIKRIQ LSTFRONSIG IVPCCHNLFC MECAVRICER TOPECPVCHI TAAQAIRIES NTTECVPVPT SERVAEIVGR PYRVVGLVVG WRVHOPGCKP SSSSAKARA PCQVTIRVRV AAIDSRYSDA TSVLESSASS MARIRIKGSS LWAGQENATP ENDFLAGSPD GAAFGVAPAL